

SEQUENCE LISTING

<110> Yamamoto, Hiroshi
Konishi, Noboru

<120> A method for decision of prostate tumor

<130> 09680

<150> JP 2004-47036

<151> 2004-02-23

<160> 5

<170> PatentIn version 3.2

<210> 1

<211> 1520

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (407).. (1267)

<400> 1

```

aggtcacaga ctgcggagtg ggtcaggggc tgcgagggt gccccaagtc ctaccgggtt      60
tgcaacgggcg cgcccggtc cgcccgcaag tgcgccttc tgacttactg ctgggtgcgc      120
ggggctgggg gtgcgagtac caccctgaa gtctcttct gggcgacctc cggggcctca      180
ttctaggcct ccttaagag aaggatctaa attaggaaaa ggaagtgcc ttatcacga      240
ccaagctctt ccacctgcgg agctcgctta gtctgcacct caaccgtgcg gaaagtgact      300
gccctgttta ctgaggaaaa actggggctc agaaagatac catggagtag tttgaaacag      360
gaacaaaatc ttctgaaagc tcggagcaga agcctttttg gtcaac atg gag gaa      415
                                   Met Glu Glu
                                   1
aaa aga cgg cga gcc cga gtt cag gga gcc tgg gct gcc cct gtt aaa      463
Lys Arg Arg Arg Ala Arg Val Gln Gly Ala Trp Ala Ala Pro Val Lys
   5              10              15
agc cag gcc att gct cag cca gct acc act gct aag ago cat ctc cac      511
Ser Gln Ala Ile Ala Gln Pro Ala Thr Thr Ala Lys Ser His Leu His
  20              25              30              35
cag aag cct gcc cag acc tgg aag aac aaa gag cat cat ctc tct gac      559
Gln Lys Pro Gly Gln Thr Trp Lys Asn Lys Glu His His Leu Ser Asp
   40              45              50
aga gag ttt gtg ttc aaa gaa cct cag cag gta gta cgt aga gct cct      607
Arg Glu Phe Val Phe Lys Glu Pro Gln Gln Val Val Arg Arg Ala Pro
   55              60              65
gag cca cga gtg att gac aga gag ggt gtg tat gaa atc ago ctg tca      655
Glu Pro Arg Val Ile Asp Arg Glu Gly Val Tyr Glu Ile Ser Leu Ser
   70              75              80
ccc aca ggt gta tct agg gtc tgt ttg tat cct gcc ttt gtt gac gtg      703
Pro Thr Gly Val Ser Arg Val Cys Leu Tyr Pro Gly Phe Val Asp Val
   85              90              95
aaa gaa gct gac tgg ata ttg gaa cag ctt tgt caa gat gtt ccc tgg      751
Lys Glu Ala Asp Trp Ile Leu Glu Gln Leu Cys Gln Asp Val Pro Trp
  100              105              110              115
aaa cag agg acc gcc atc aga gag gat ata act tat cag caa cca aga      799
Lys Gln Arg Thr Gly Ile Arg Glu Asp Ile Thr Tyr Gln Gln Pro Arg
   120              125              130
ctt aca gca tgg tat gga gaa ctt cct tac act tat tca aga atc act      847

```

Leu Thr Ala Trp Tyr Gly Glu Leu Pro Tyr Thr Tyr Ser Arg Ile Thr
 135 140 145
 atg gaa cca aat cct cac tgg cac cct gtg ctg cgc aca cta aag aac 895
 Met Glu Pro Asn Pro His Trp His Pro Val Leu Arg Thr Leu Lys Asn
 150 155 160
 cgc att gaa gag aac act ggc cac acc ttc aac tcc tta ctc tgc aat 943
 Arg Ile Glu Glu Asn Thr Gly His Thr Phe Asn Ser Leu Leu Cys Asn
 165 170 175
 ctt tat cgc aat gag aag gac agc gtg gac tgg cac agt gat gat gaa 991
 Leu Tyr Arg Asn Glu Lys Asp Ser Val Asp Trp His Ser Asp Asp Glu
 180 185 190 195
 ccc tca cta ggg agg tgc ccc att att gct tca cta agt ttt ggt gcc 1039
 Pro Ser Leu Gly Arg Cys Pro Ile Ile Ala Ser Leu Ser Phe Gly Ala
 200 205 210
 aca cgc aca ttt gag atg aga aag aag cca cca cca gaa gag aat gga 1087
 Thr Arg Thr Phe Glu Met Arg Lys Lys Pro Pro Pro Glu Glu Asn Gly
 215 220 225
 gac tac aca tat gtg gaa aga gtg aag ata ccc ttg gat cat ggg acc 1135
 Asp Tyr Thr Tyr Val Glu Arg Val Lys Ile Pro Leu Asp His Gly Thr
 230 235 240
 ttg tta atc atg gaa gga gcg aca caa gct gac tgg cag cat cga gtg 1183
 Leu Leu Ile Met Glu Gly Ala Thr Gln Ala Asp Trp Gln His Arg Val
 245 250 255
 ccc aaa gaa tac cac tct aga gaa ccg aga gtg aac ctg acc ttt cgg 1231
 Pro Lys Glu Tyr His Ser Arg Glu Pro Arg Val Asn Leu Thr Phe Arg
 260 265 270 275
 aca gtc tat cca gac cct cga ggg gca ccc tgg tga cgtcagagct 1277
 Thr Val Tyr Pro Asp Pro Arg Gly Ala Pro Trp
 280 285
 ttgagagaga agcttcactg aaacggagca aacctccac tgagaagcca cttcaagagg 1337
 ctggtgctgc tagatctcat gatgtggctg ttgggaagat ggtggggttt gtttgcagc 1397
 ttggagtcct attaaatgaa agccagcaac tcatgttgg aataggctcta ctgtgggaac 1457
 agttatccct aaccacagct caaaatcgct atcatcttta ggcaaattaa aatctatgtg 1517
 gca 1520

<210> 2
 <211> 286
 <212> PRT
 <213> Homo sapiens

<400> 2

Met Glu Glu Lys Arg Arg Arg Ala Arg Val Gln Gly Ala Trp Ala Ala
 1 5 10 15
 Pro Val Lys Ser Gln Ala Ile Ala Gln Pro Ala Thr Thr Ala Lys Ser
 20 25 30
 His Leu His Gln Lys Pro Gly Gln Thr Trp Lys Asn Lys Glu His His
 35 40 45
 Leu Ser Asp Arg Glu Phe Val Phe Lys Glu Pro Gln Gln Val Val Arg
 50 55 60
 Arg Ala Pro Glu Pro Arg Val Ile Asp Arg Glu Gly Val Tyr Glu Ile
 65 70 75 80

Ser Leu Ser Pro Thr Gly Val Ser Arg Val Cys Leu Tyr Pro Gly Phe
85 90 95

Val Asp Val Lys Glu Ala Asp Trp Ile Leu Glu Gln Leu Cys Gln Asp
100 105 110

Val Pro Trp Lys Gln Arg Thr Gly Ile Arg Glu Asp Ile Thr Tyr Gln
115 120 125

Gln Pro Arg Leu Thr Ala Trp Tyr Gly Glu Leu Pro Tyr Thr Tyr Ser
130 135 140

Arg Ile Thr Met Glu Pro Asn Pro His Trp His Pro Val Leu Arg Thr
145 150 155 160

Leu Lys Asn Arg Ile Glu Glu Asn Thr Gly His Thr Phe Asn Ser Leu
165 170 175

Leu Cys Asn Leu Tyr Arg Asn Glu Lys Asp Ser Val Asp Trp His Ser
180 185 190

Asp Asp Glu Pro Ser Leu Gly Arg Cys Pro Ile Ile Ala Ser Leu Ser
195 200 205

Phe Gly Ala Thr Arg Thr Phe Glu Met Arg Lys Lys Pro Pro Pro Glu
210 215 220

Glu Asn Gly Asp Tyr Thr Tyr Val Glu Arg Val Lys Ile Pro Leu Asp
225 230 235 240

His Gly Thr Leu Leu Ile Met Glu Gly Ala Thr Gln Ala Asp Trp Gln
245 250 255

His Arg Val Pro Lys Glu Tyr His Ser Arg Glu Pro Arg Val Asn Leu
260 265 270

Thr Phe Arg Thr Val Tyr Pro Asp Pro Arg Gly Ala Pro Trp
275 280 285

<210> 3
<211> 861
<212> DNA
<213> Homo sapiens

<400> 3
atggaggaaa aaagacggcg agcccgagtt cagggagcct gggctgcccc tgttaaaagc 60
caggccattg ctcagccagc taccactgct aagagccatc tccaccagaa gcctggccag 120
acctggaaga acaaagagca tcattctctc gacagagagt ttgtgttcaa agaacctcag 180
caggtagtac gtagagctcc tgagccacga gtgatigaca gagagggtgt gtatgaaatc 240
agcctgtcac ccacaggtgt atctagggtc tgtttgtatc ctggctttgt tgacgtgaaa 300
gaagctgact ggatattgga acagctttgt caagatgttc cctggaaaca gaggaccggc 360
atcagagagg atataactta tcagcaacca agacttacag catggtatgg agaacttctc 420
tacaattatt caagaatcac tatggaacca aatcctcact ggcaccctgt gctgcgcaca 480
ctaaagaacc gcattgaaga gaacactggc cacaccttca actccttact ctgcaatctt 540

tatcgcaatg agaaggacag cgtggactgg cacagtgatg atgaaccctc actagggagg 600
 tgccccatta ttgcttcact aagttttggt gccacacgca catttgagat gagaaagaag 660
 ccaccaccag aagagaatgg agactacaca tatgtggaaa gagtgaagat acccttggat 720
 catgggacct tgtaatcat ggaaggagcg acacaagctg actggcagca togagtgcc 780
 aaagaatacc actctagaga accgagagtg aacctgacct ttoggacagt ctatccagac 840
 cctcgagggg caccctgggtg a 861

<210> 4
 <211> 21
 <212> DNA
 <213> Artificial

<220>
 <223> Oligonucleotide designed to act as PCR primer for detection of
 PCA-1 gene

<400> 4
 ctgaaagctc ggagcagaag c 21

<210> 5
 <211> 18
 <212> DNA
 <213> Artificial

<220>
 <223> Oligonucleotide designed to act as PCR primer for detection of
 PCA-1 gene

<400> 5
 ggtctactgt gggaacag 18